

FIGURE 1

ř.

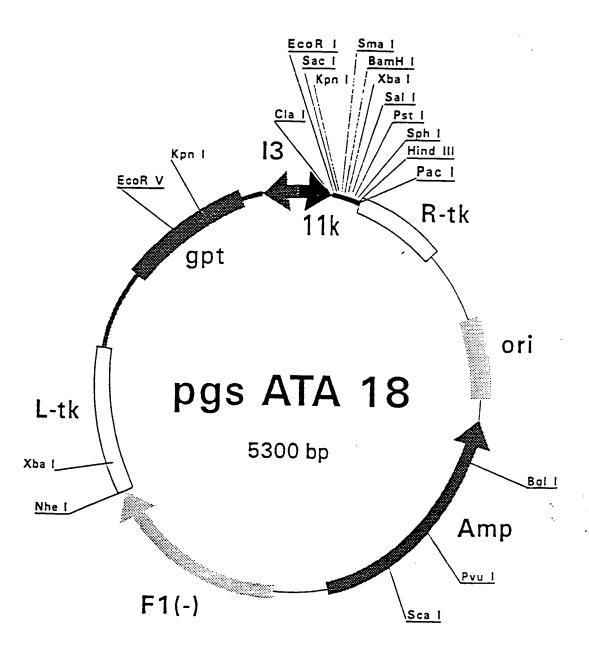


FIGURE 2

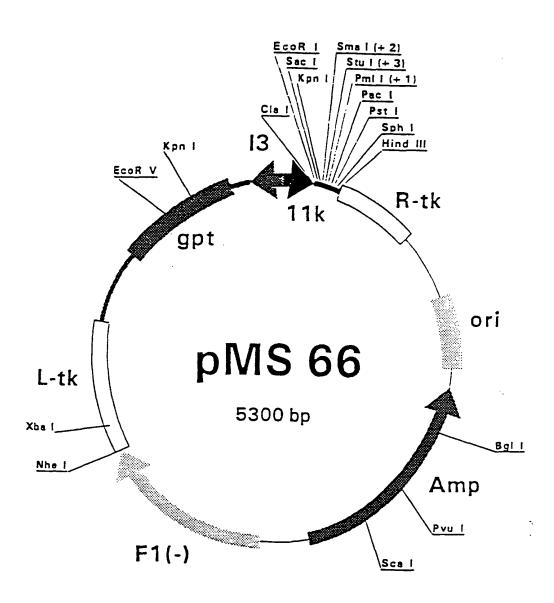


FIGURE 3

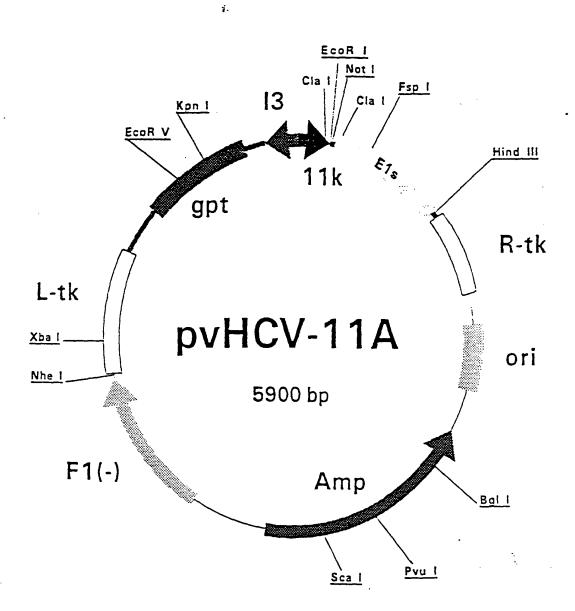
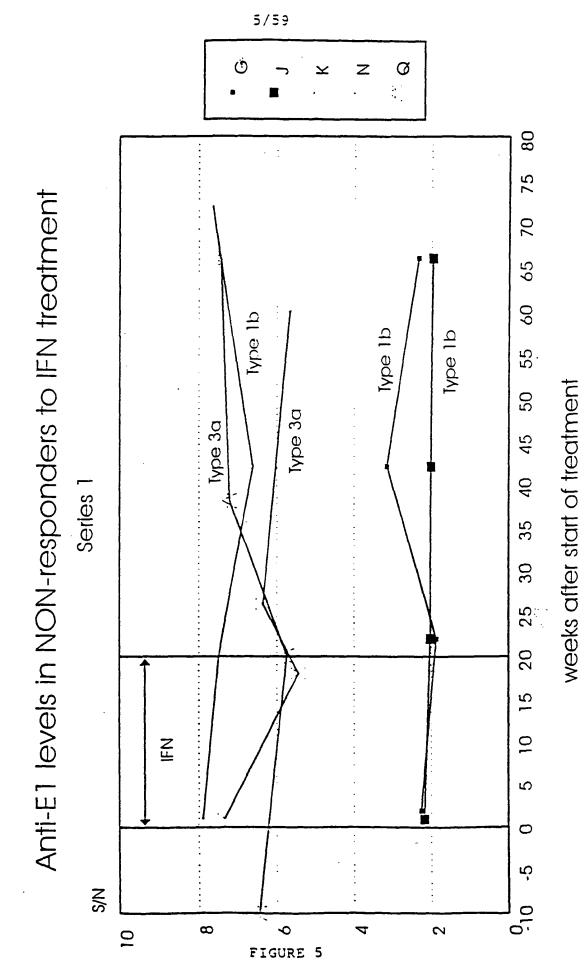
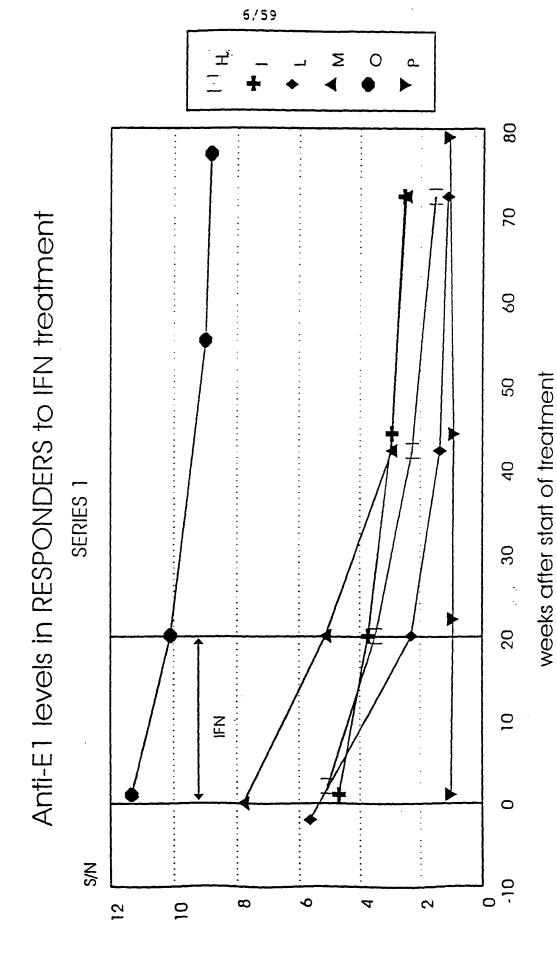
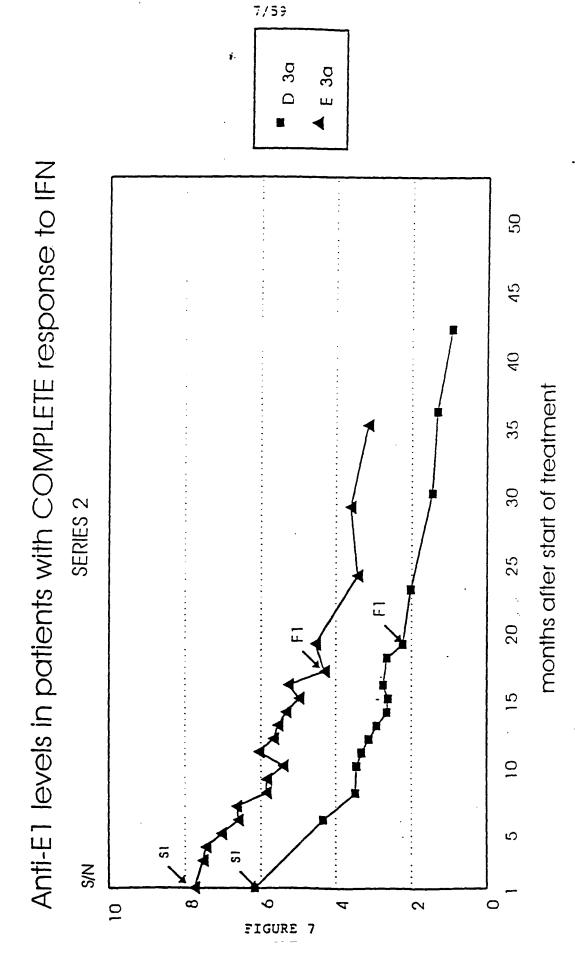


FIGURE 4

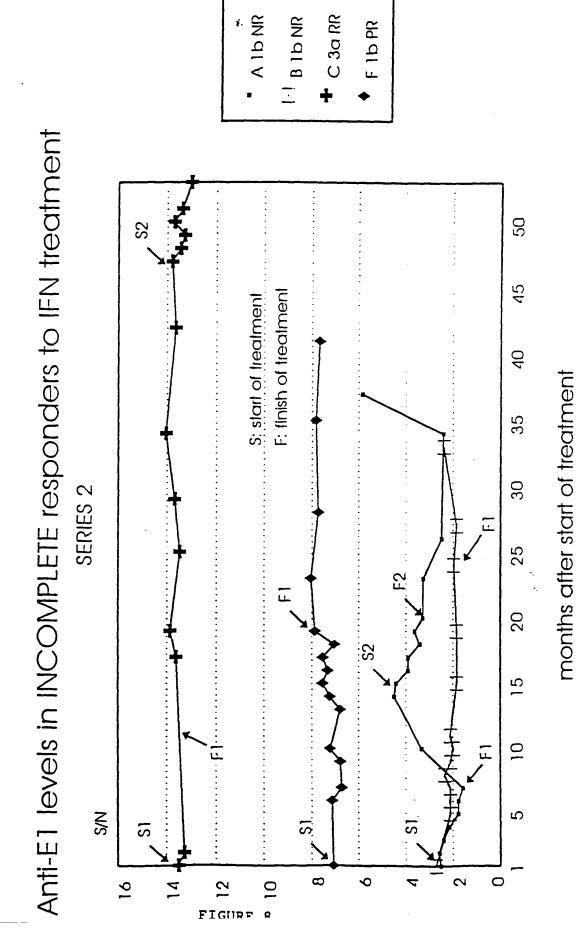
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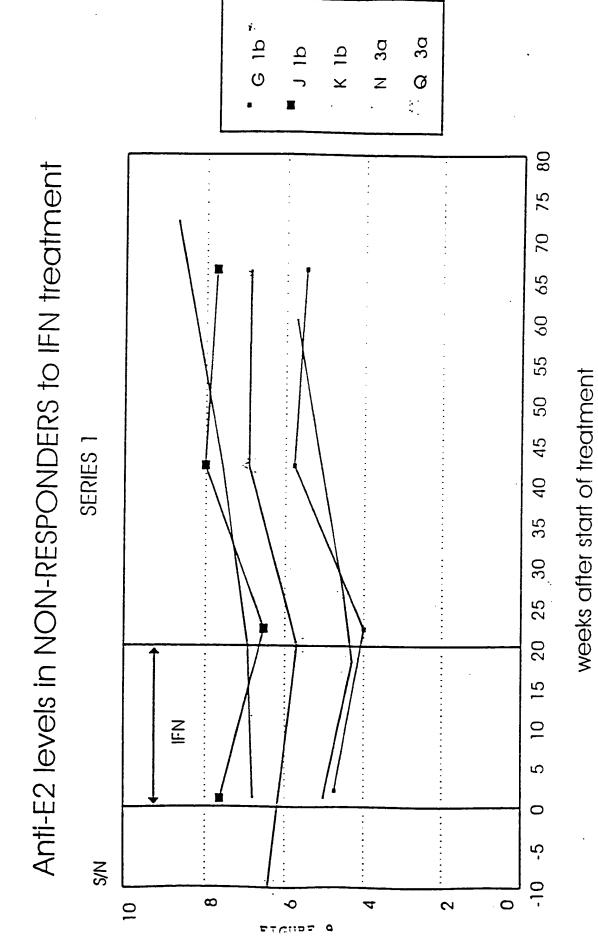


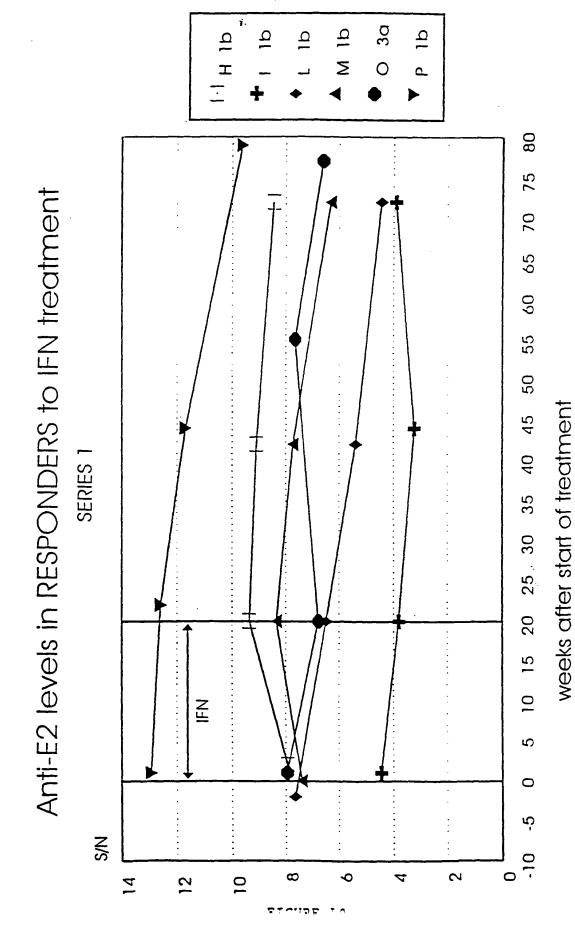




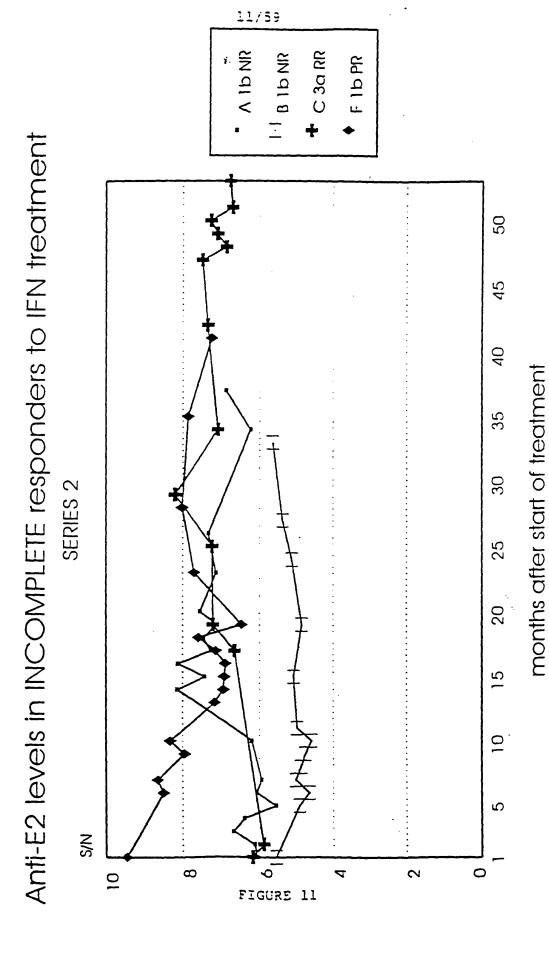








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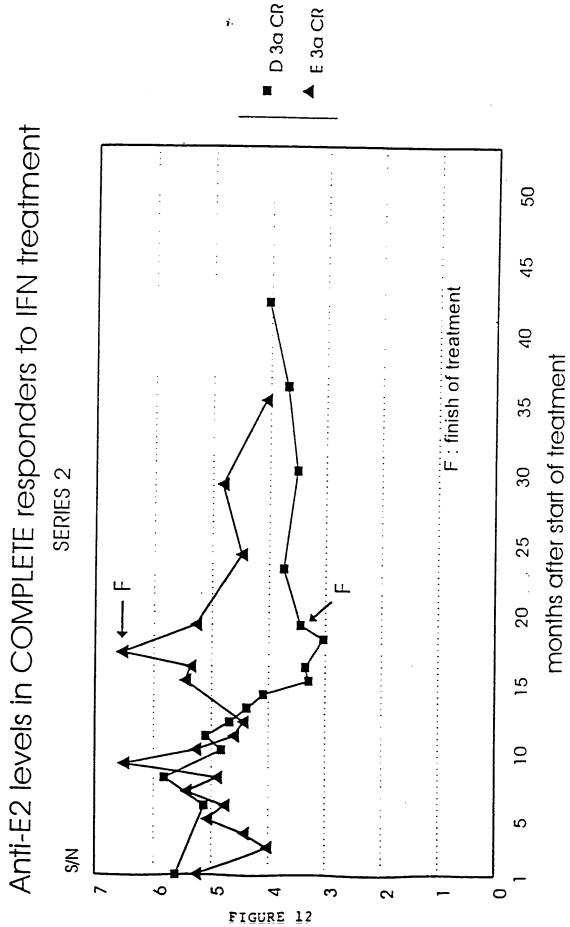


FIGURE 13

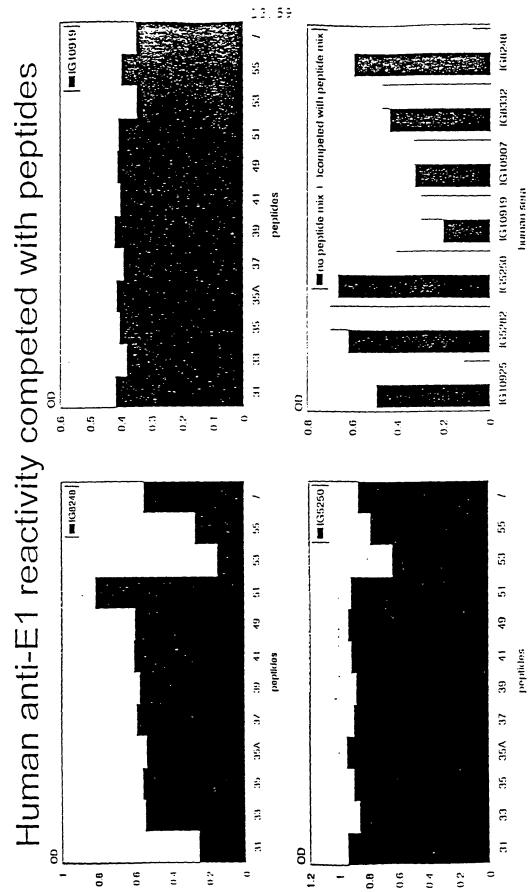
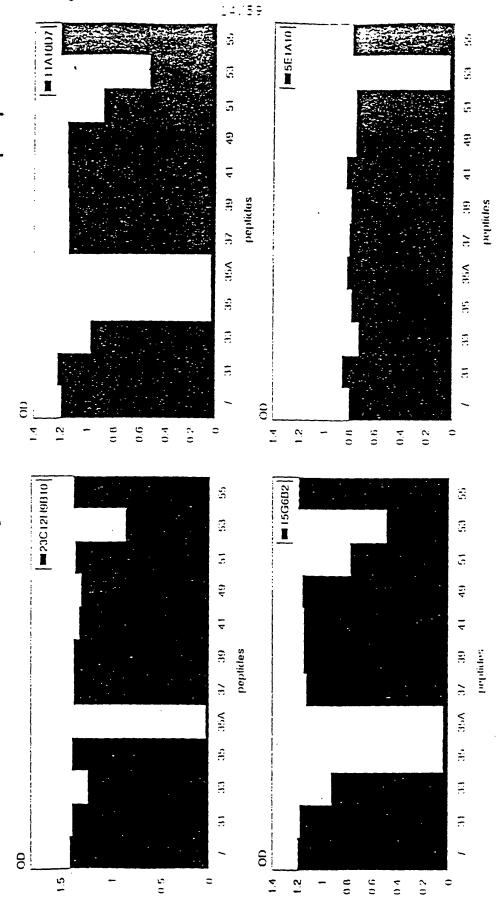


FIGURE 14

Competition of reactivity of anti-E1 Mabs with peptides

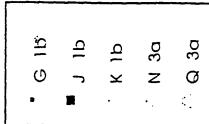


weeks after start of treatment

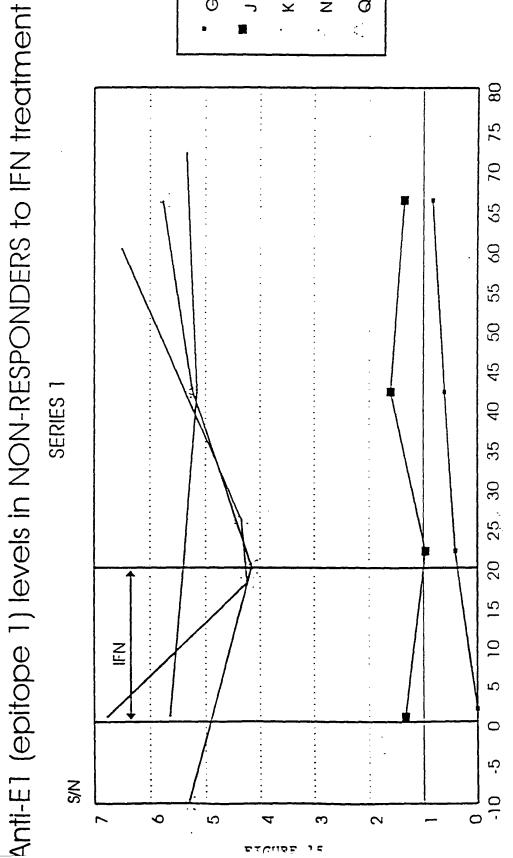
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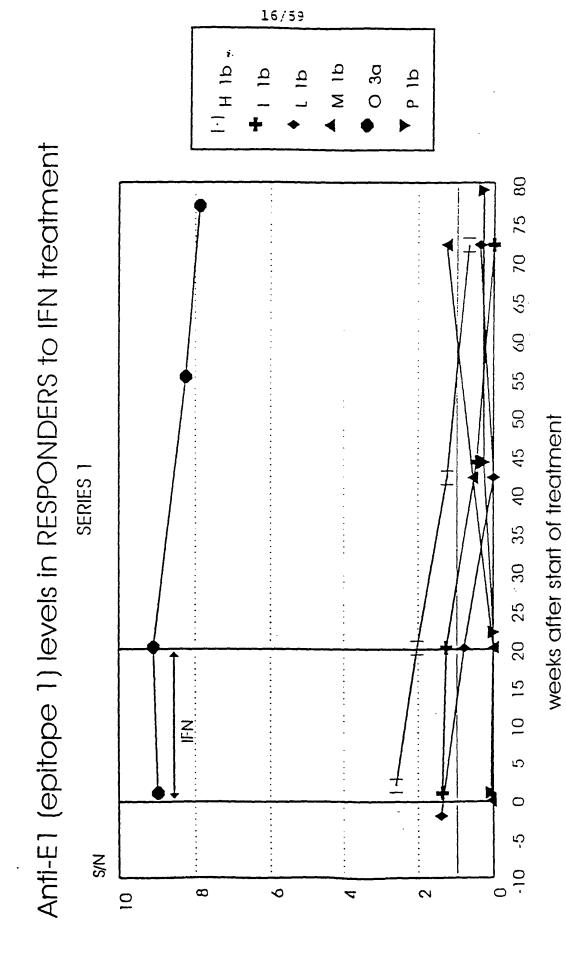


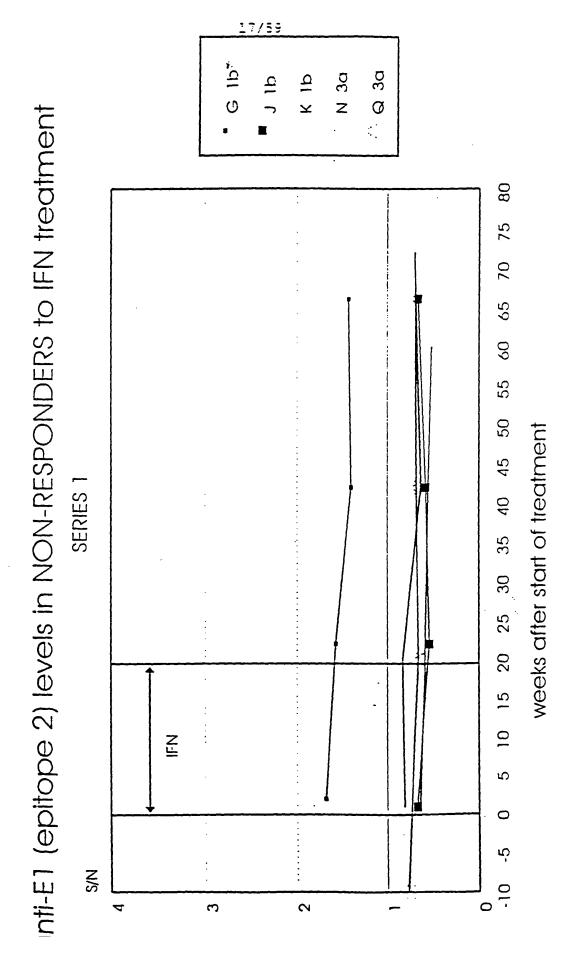


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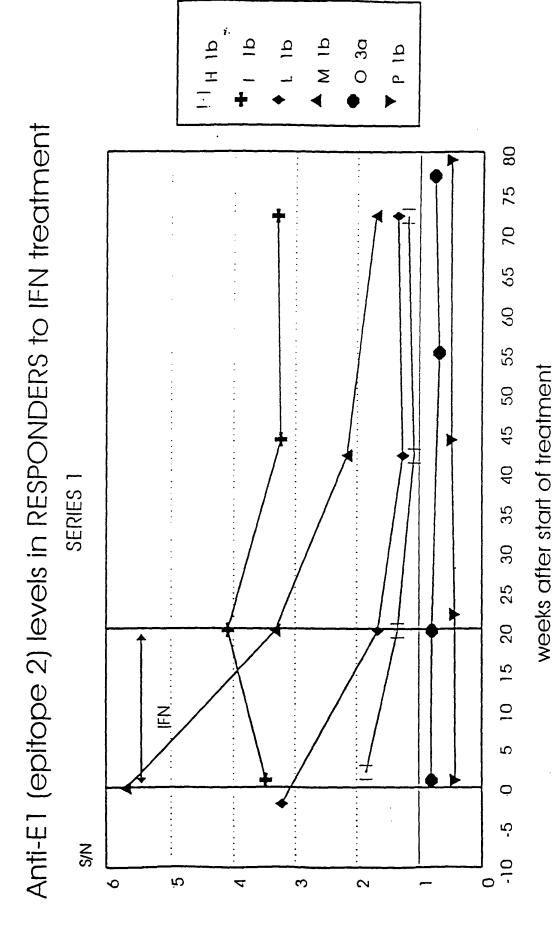
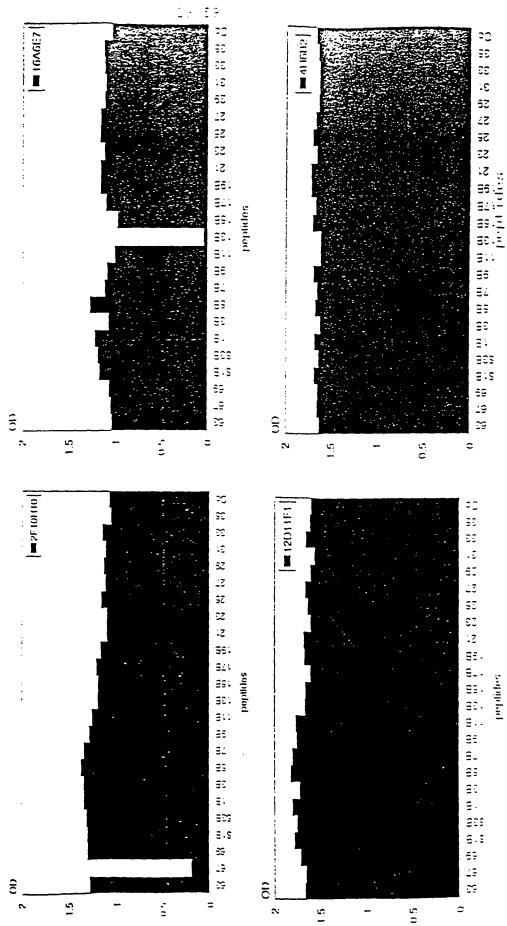


FIGURE 19 Competition of reactivity of anti-E2 Mabs with peptides



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FIGURE 20

Human anti-E2 reactivity competed with peptides

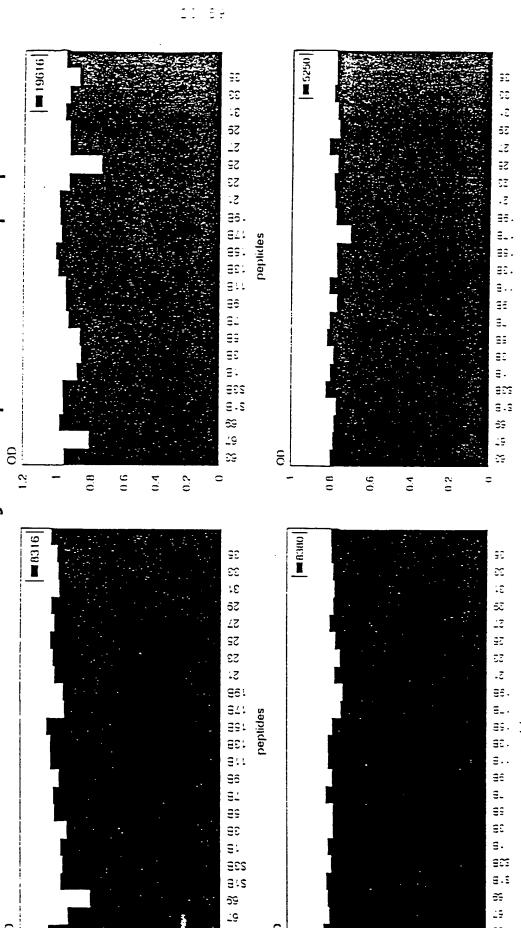


Figure 21

5' GGCATGCAAGCTTAATTAATT3' (SEQ ID NO 1)
3'ACGTCCGTACGTTCGAATTAATTAATCGA5' (SEQ ID NO 94)

SEQ ID NO 3 (HCCI9A)

SEQ ID NO 5 (HCCI10A)



SEQ ID NO 7 (HCCI11A)

SEQ ID NO 9 (HCCI12A)

SEQ ID NO 11 (HCCI13A)



GCCCTGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTC
GTTGGGGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCTGTTTT
CCTTGTTTCCCAGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAT
GAACTGGTAATAG

SEQ ID NO 13 (HCCI17A)

SEQ ID NO 15 (HCPr51)
ATGCCGGTTGCTCTTTCTCTATCTT

SEQ ID NO 16 (HCPr52)

ATGTTGGGTAAGGTCATCGATACCCT

SEQ ID NO 17 (HCPr53)
CTATTAGGACCAGTTCATCATCATATCCCA

SEQ ID NO 18 (HCPr54)
CTATTACCAGTTCATCATCATATCCCA

SEQ ID NO 19 (HCPr107)

ATACGACGCCACGTCGATTCCCAGCTGTTCACCATC

SEQ ID NO 20 (HCPr108)
GATGGTGAACAGCTGGGAATCGACGTGGCGTCGTAT

SEQ ID NO 21 (HCCI37)

SEQ ID NO 23 (HCCI38)

SEQ ID NO 25 (HCC139)

TAG

ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTCTCT



CAACGTGTCCGGGATGTACCATGTCACGAACGACTGCCCAACTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACCACCCCGGGTGCCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGAACTGGTCGCCTACAACGGCCCTGGTGTAT
CGCAGCTGCTCCGGATCCTCAATAG

SEQ ID NO 27 (HCCI40)

SEQ ID NO 29 (HCCI62)

ATGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTATATCC
CGCTCGTAGGCGGCCCCATTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGT
CCTTGAGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCT
TTATTCTTGCTCTTCTCTCGTGTCTGACCGTTCCGGCCTCTGCAGTTCCCTACCGAAATG
CCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCA
GATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCATGACAGGTAATGTGA
GTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCAC
GGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCGGGAGGGGCTGCCCTCTGCTCCGCG
TTATACGTAGGAGACGCGTGTGGGGCACTATTCTTGGTAGGCCAAATGTTCACCTATA
GGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGCCATGT
TACCGGCCACCGGATGGCATGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 33 (HCPr109) TGGGATATGATGATGAACTGGTC

SEQ ID NO 34 (HCPr72)

CTATTATGGTGGTAAKGCCARCARGAGCAGGAG

SEQ ID NO 35 (HCCL22A)

CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCACCTTCACCATCTTCAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCG
AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGATACTGCCCTGTTCCTTCACCACCCCTGCCGGCCCTATCCA
CCGGCCTGATCCACCTCCATCAGAACATCGTGGACGTGCAATACCTGTACGGTGTAGG
GTCGGCGGTTGTCTCCCTTGTCATCAAATGGGAGTATGTCCTGTTGCTCTTCCTT
GGCAGACGCGCGCATCTGCGCCTGCTTATGGATGATGCTGATAGCTCAAGCTGAG
GCCGCCTTAGAGAACCTGGTGGTCCTCAATGCGGCGGCCGTGGCCGGGGCGCATGGC
ACTCTTTCCTTCCTTGTGTTCTTCTGTGCTGCCTGGTACATCAAGGGCAGGCTGTCCC
TGGTGCGGCATACGCCTTCTATGGCGTGTCCCTGCTTCTGCTGCCTTACC
CACCACGAGCTTATGCCTAGTAA

SEC ID NO 37 (HCCI41)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGCCCATTGGGGAGTCCTGGCGG CCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGATGCTACTCT TTGCCGGCGTCGACGGGCATACCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCA GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACAC AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG CGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC GTGTGGTATTGTACCCGCGTCTCAGGTGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC CGACTCGGATGTGCTGATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGC TGTACATGGATGAATGGCACTGGGGTTCACCAAGACGTGTGGGGGCCCCCCGTGCAACA CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT TAGGATGTACGTGGGGGGGGGGGGGGCACAGGTTCGAAGCCGCATGCAATTGGACTCG AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG TCTACAACAGAGTGGCAGAGTTAATTAATTAG

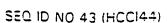
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SEQ ID NO 41 (HCCI43)

ATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG GGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT CTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC TATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCG CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC ATTCTCAACACACGCGGCCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG GCACTGGGTTCACCAAGACGTGTGGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCA ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG GGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGG CAGAGCTTAATTAATTAG





ATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG GGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT CTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC TATTCTACAACACACAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCG CTCCATCGACAGGTTCGCTGAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC GACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTG ATTCTCAACACGCGGCGCGCGCGGGGGCAACTGGTTCGGCTGTACATGGATGAATG GCACTGGGTTCACCAAGACGTGTGGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCA ACAACACETTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG GGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGTCTACAACAGGTGAT CGAGGGCAGACACCATCACCATCACTAATAG

SEQ ID NO 45 (HCCL64)

PCT/EP95/03031

TGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGA
GGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATA
CTGCCCTGTTCCTTCACCACCCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCA
GAACATCGTGGACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTC
ATCAAATGGGAGTATGTCCTGTTGCTCTTCCTTCTCCTGGCAGACGCGCGCATCTGCGC
CTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTG
GTCCTCAATGCGGCGGCCGTGGCCGGGGCGCATGCCCTTCTTC
CTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCGCCATACGCCTTCTAT
GGCGTGTGGCCGCTGCTCCTGCTTCTCTTCCTTAGCCTAGTAA

SEQ ID NO 47 (HCCI65)

AATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG GGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT ATCTTCCTCTTGGCTTTGCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG CAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTAT GAGGCAGCGGACATGATCATGCACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG TTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCA CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG CCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACG GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGG GGGCCCATTGGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGGC TAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGCGTGTCAG GAGGGGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGC TCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACTGCCCT GAACTGCAACGACTCCCCAAACAGGGTTCTTTGCCGCACTATTCTACAAACACAAA TTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCG CTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGGCCCTA CTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGT CCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGGACGACCGATCGGTTTGGTGT CCCCACGTATAACTGGGGGGGGAACGACTCGGATGTGCTGATTCTCAACAACACGCGG CCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTCACCAAGA CGTGTGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCAACACACCTTGACCTGCC

SEQ ID NO 49 (HCCI66)

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCA CAGGACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGC GCAGGGGCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAAC CTCGTGGGAGGCGACAACCTATCCCCAAGGCTCGCCGACCCGAGGGTAGGGCCTGGG CTCAGCCCGGGTACCCTTGGCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATG GCTCCTGTCACCCGCGGCTCTCGGCCTAGTTGGGGCCCTACAGACCCCCGGCGTAGG TCGCGTAATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGG GGTACATTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGG CGTCCGGGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCT TTCTCTATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAA GTGCGCAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTG GAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCC AGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTT TCTGTTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTG TTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATC CCGGCCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTAC AACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTG GCGGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACT GGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGCGT GTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTTAGCCCCGGG

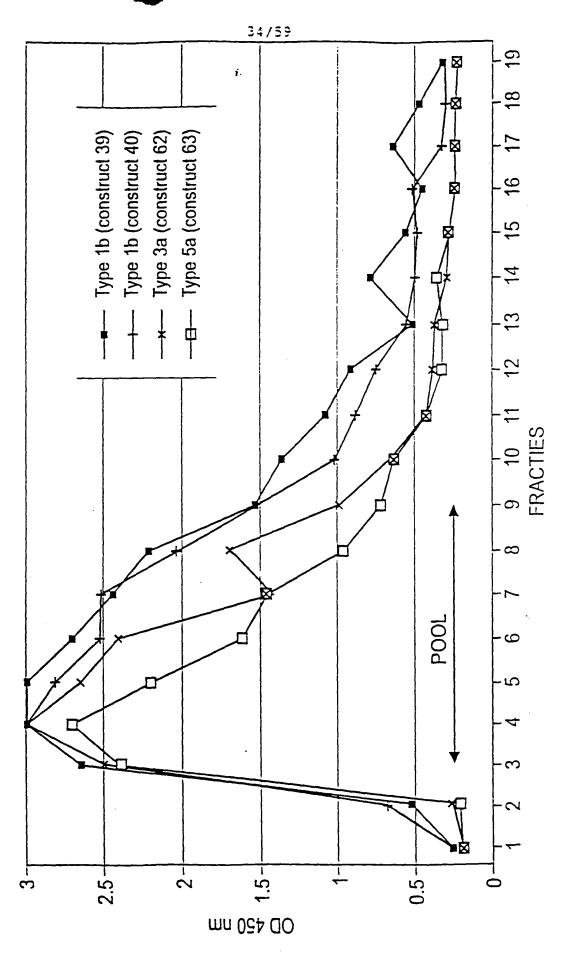
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Figure 22

OD measured at 450 nm construct

Fraction	volume dilution	39 Typ e Ih	40 Typ= Ih	62 Type 3a	63 Type 5a
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	23 ml 1/20 UGH 23 ml 1/20 0.4 ml 1/200	2.517 0.087 0.102 0.396 2.627 3 3 2.694 2.408 2.176 1.461 1.286 0.981 0.812 0.812 0.873 0.653 0.441 0.321 0.525 0.351	1.954 0.085 0.051 0.550 2.603 2.967 2.810 2.499 2.481 1.970 1.422 0.926 0.781 0.650 0.432 0.371 0.348 0.374 0.186 0.171	1.426 0.176 0.048 0.090 2.481 3 2.640 1.359 0.347 1.624 0.887 0.543 0.294 0.249 0.239 0.145 0.151 0.098 0.099 0.083	1.142 0.120 0.050 0.067 2.372 2.694 2.154 1.561 1.390 0.865 0.604 0.519 0.294 0.199 0.209 0.184 0.151 0.106 0.108 0.090
19		0.192	0.164	0.084	0.087





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			OD measured at 450 nm construct				
Fraction	volume	dilution	39 Type 1b	40 Type 1b	62 Type 3a	63 Type 5a	
20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40	250 μl	1/200	0.072 0.109 0.279 0.093 0.080 0.251 3 3 3 2.227 0.263 0.071 0.103 0.045 0.045 0.045 0.045 0.045	0.130 0.293 0.249 0.151 0.266 0.100 1.649 3 3 3 1.921 0.415 0.172 0.054 0.045 0.045 0.047 0.045 0.047	0.096 0.084 0.172 0.297 0.438 0.457 0.722 2.526 3 2.849 1.424 0.356 0.154 0.096 0.044 0.045 0.045 0.049 0.046 0.047 0.050 0.048	0.051 0.052 0.052 0.054 0.056 0.056 0.066 0.889 2.345 2.580 1.333 0.162 0.064 0.057 0.051 0.046 0.040 0.048 0.057 0.049	

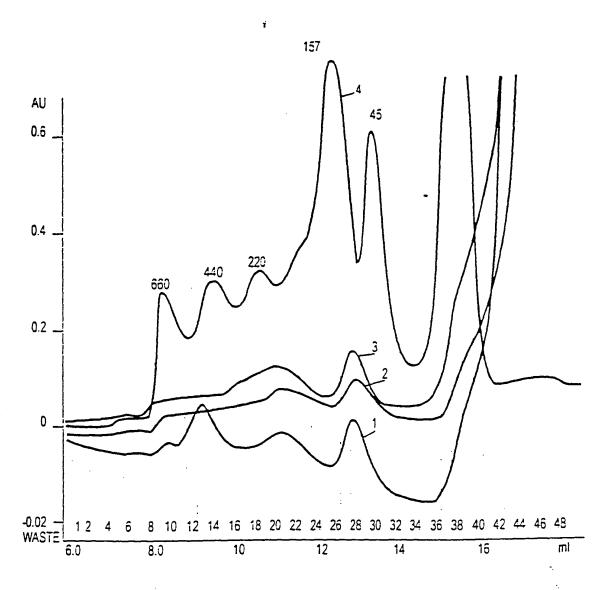


FIGURE 25

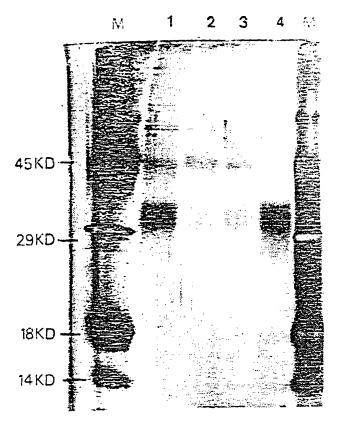


Figure 25

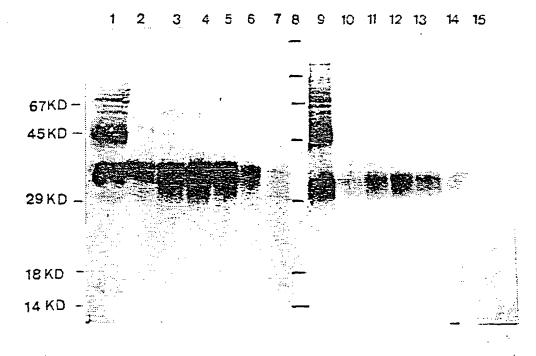


Figure 27

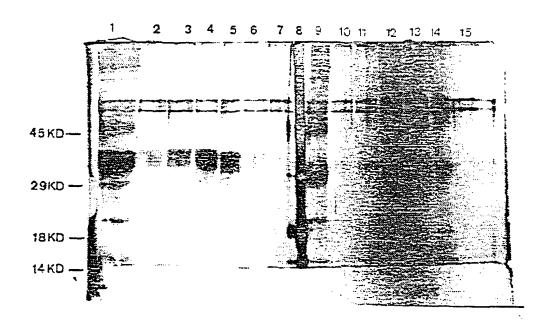
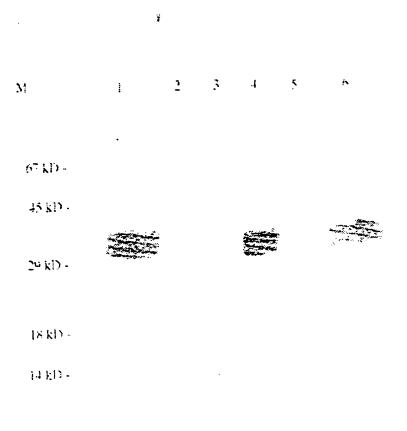


Figure 28

1



Lane 1: Crude Lysate

Lang 2: Flow through Lentil Chromatography

Lane 3: Wash with EMPIGEN Lentil Chromatography

Lane 4: Eluate Lentil Chromatography

Latte 5: Flow through during concentration lentil cluate

Lanc 6: Pool of Higher Size Exclusion Chromatography

Figure 29: Western Blot Analysis with anti-E1 mouse monoclonal 5E1A10

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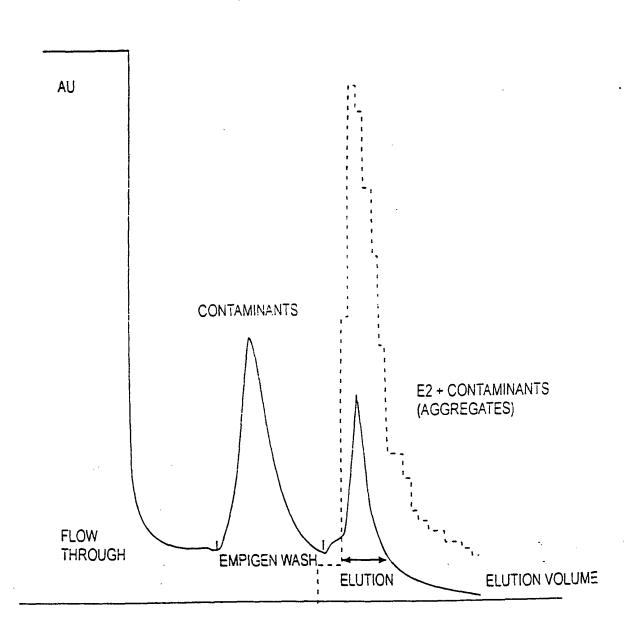
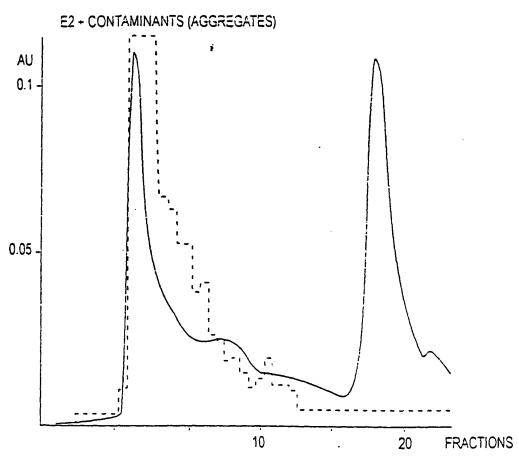


FIGURE 30

A: NON - REDUCED



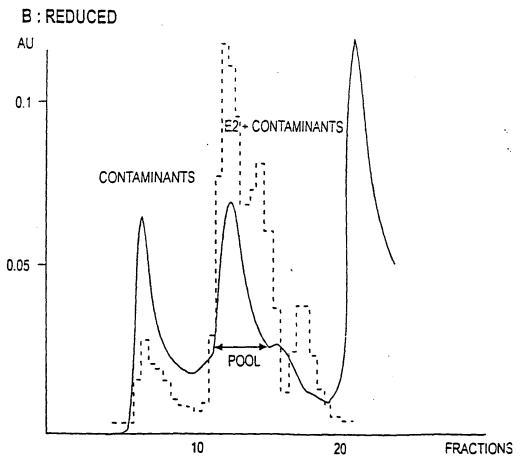


FIGURE 31

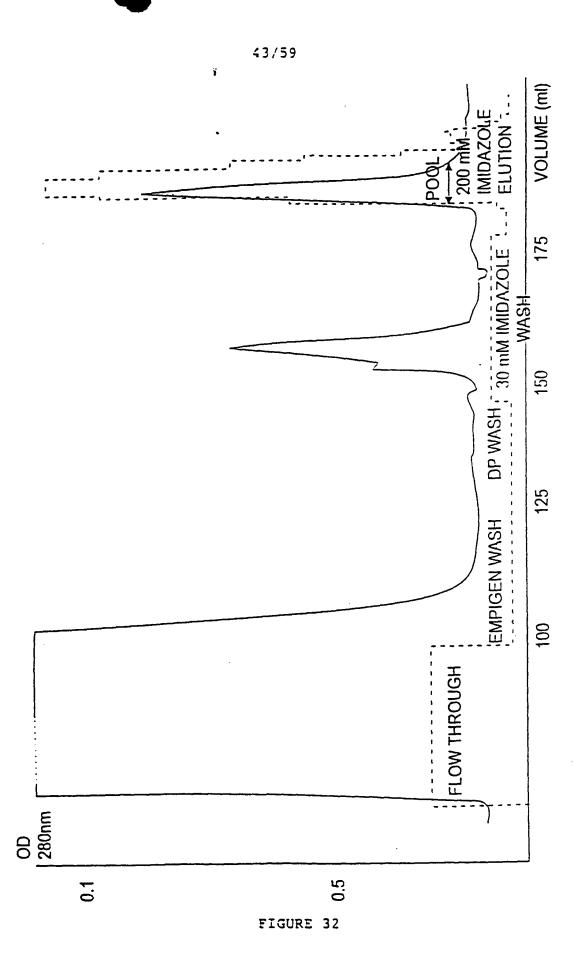
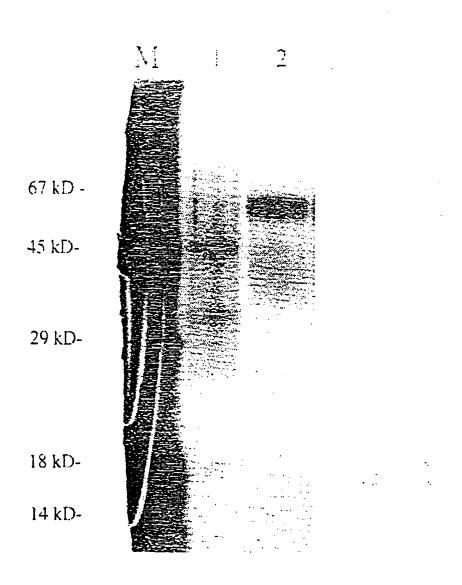
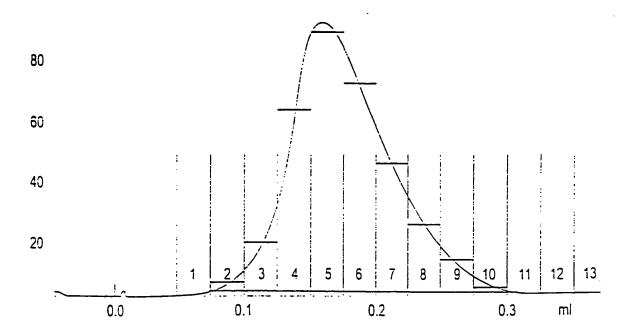


FIGURE 33: SILVER STAIN OF PURIFIED E2



- 1. 30 mM IMIDAZOLE WASH NI-IMAC
- 2. 0.5 as E2

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No.	Ret.	Peak start (ml)	Peak end (ml)	Dur (ml)	Area (ml*mAU)	Height (mAU)
1	-0.45	-0.46	-0.43	0.04	0.0976	4.579
ž	1.55	0.75	3.26	2.51	796.4167	889.377
3	3.27	3.26	3.31	0.05	0.0067	0.224
4	3.33	3.32	3.33	0.02	0.0002	0.018

Total number of detected peaks = 4
Total Area above baseline = 0.796522 ml*AU
Total area in evaluated peaks = 0.796521 ml*AU
Ratio peak area / total area = 0.999999
Total peak duration = 2.613583 ml

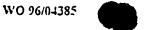
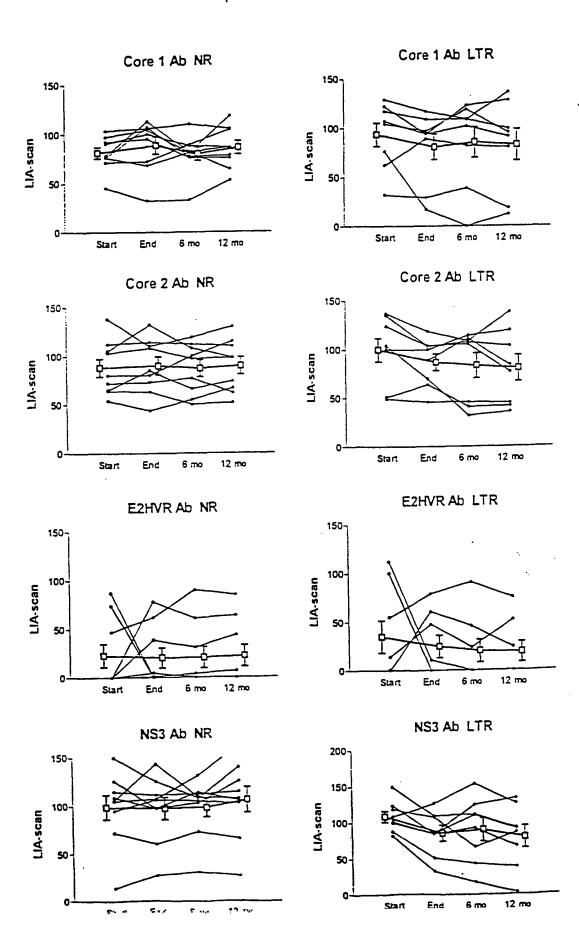


FIGURE 35A





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FIGURE 35B

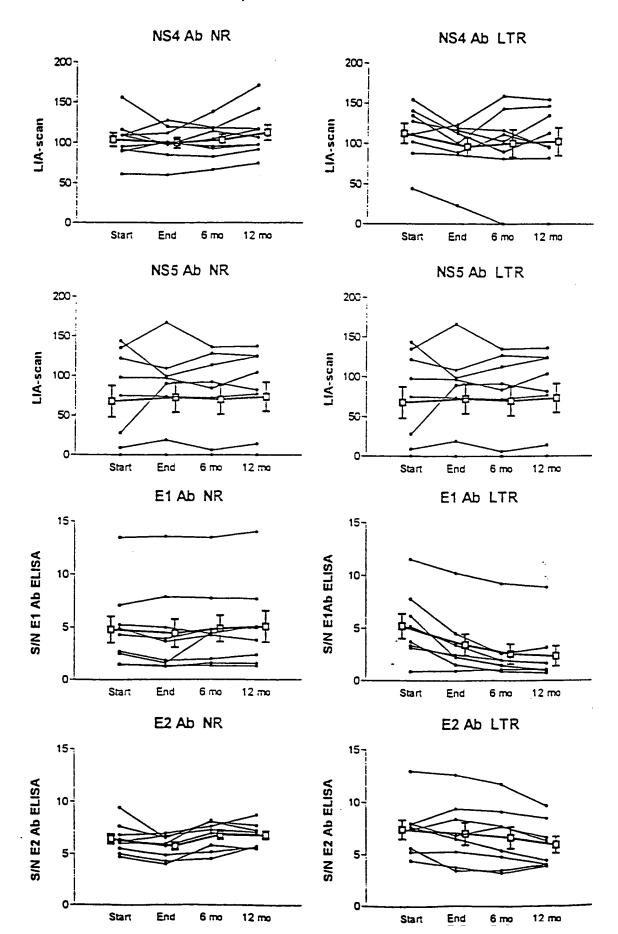
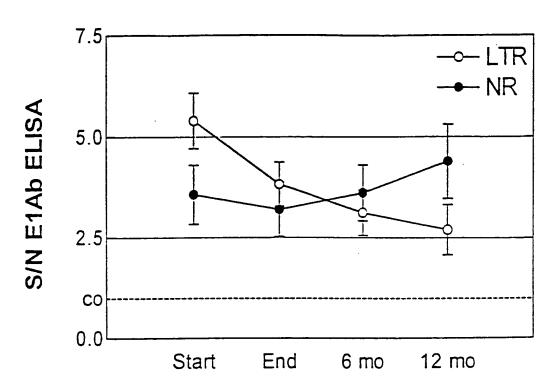


Figure 36

E1 Ab



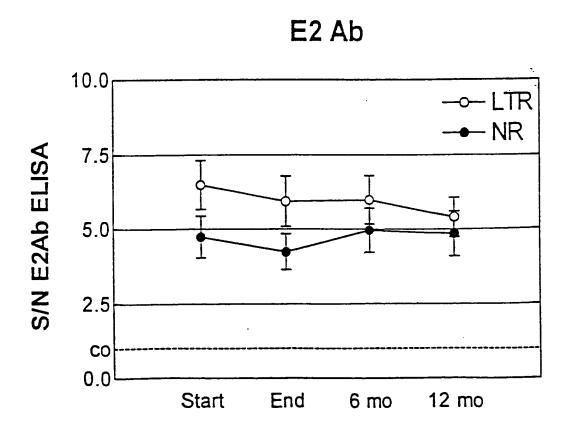


FIGURE 37

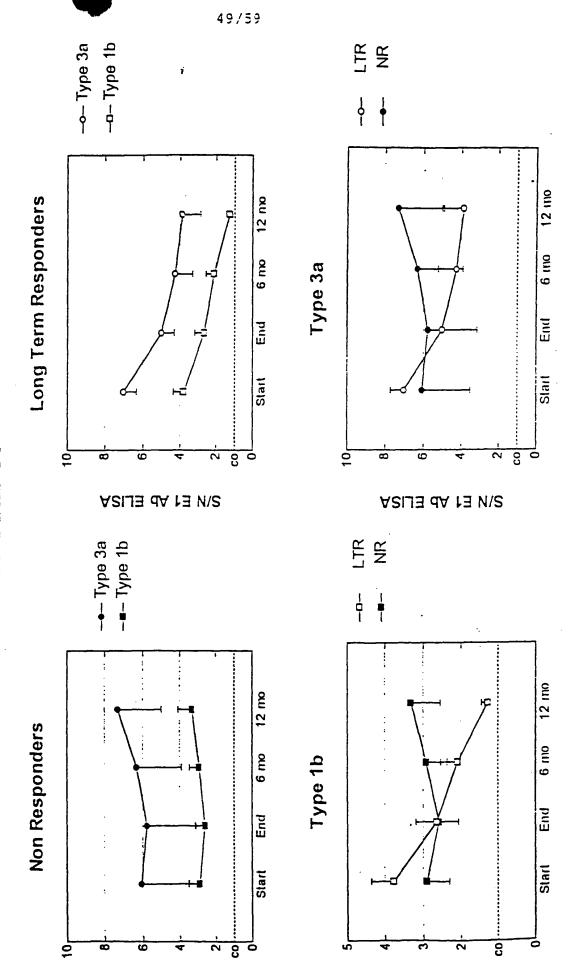
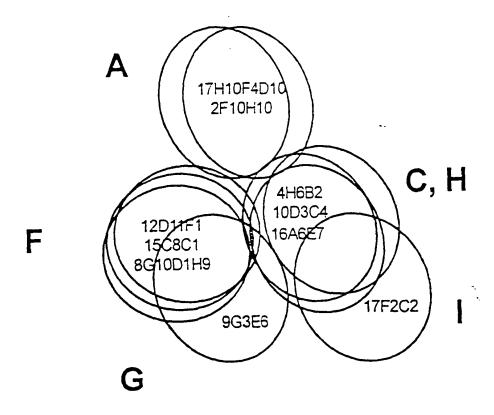
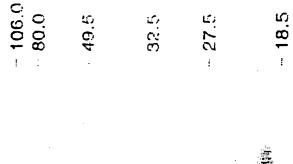
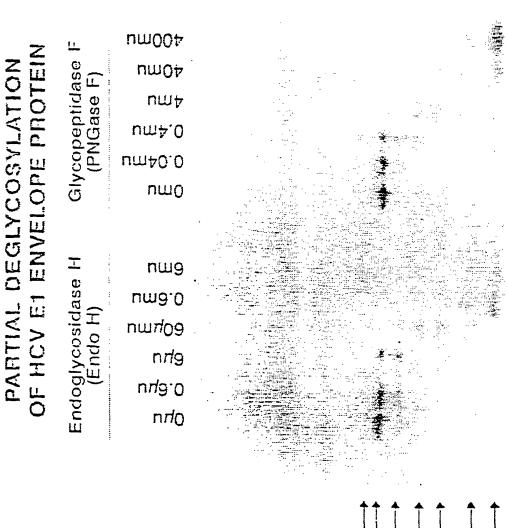


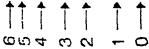
Figure 38

Relative Map Positions of anti-E2 monoclonal antibodies









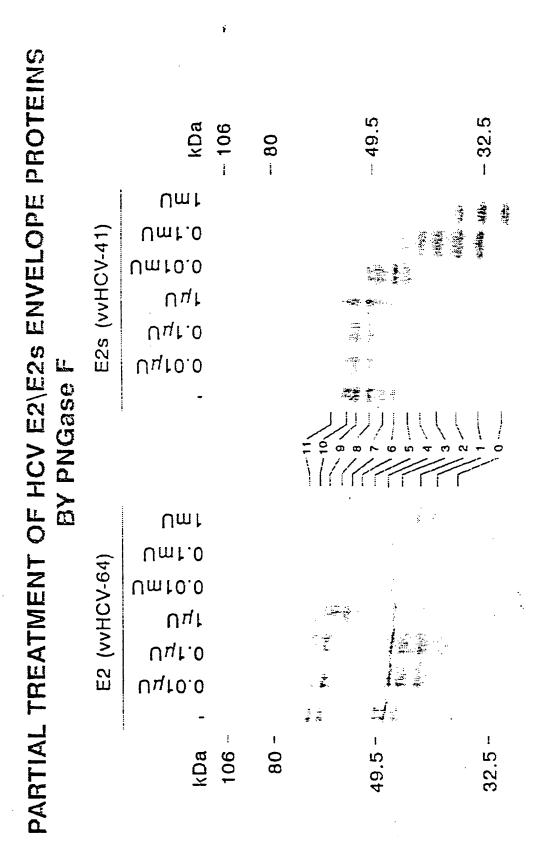
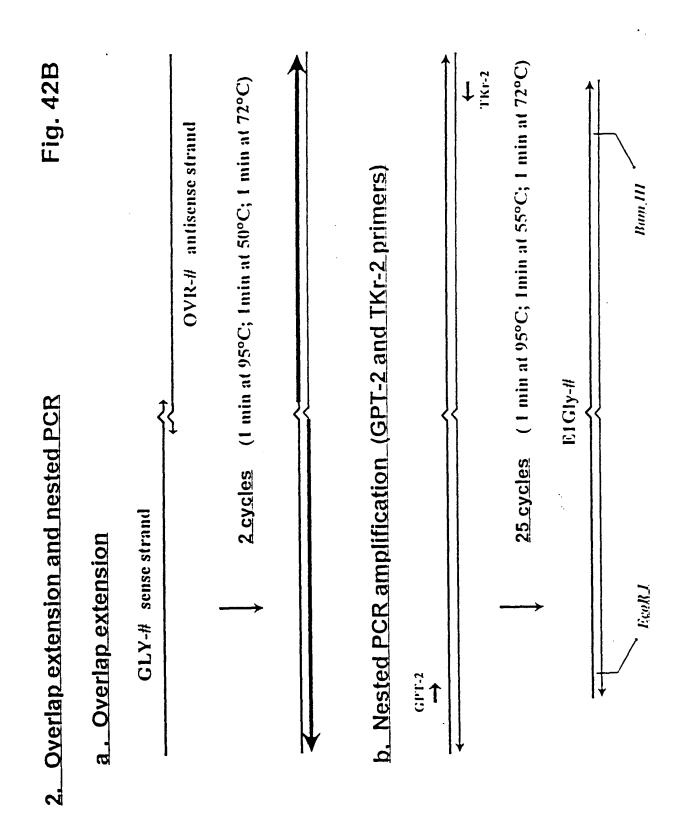


Figure 40

OVR-#

30 cycles (1 min at 95°C; 1 min at 50°C; 1 min at 72°C) In Vitro Mutagenesis of HCV E1 glycoprotein First step of PCR amplification (Gly-# and Ovr-# primers) Bautil E.1 **₹**\$ **₹** 5 Uvr-# GLY-# EcoR 1 GPT CPT Fig. 42A



In Vitro Mutagenesis of HCV E1 glycoprotein

Fig. 43

56/59 EIGly-5 EIGly-2 E1Gly-3 EIGly-6 EIGly-1 E1Gly-4 **E**2 Τ₹ 500 nd Banell Bantl 550 nt 6.30 nt <u>-</u> 770 nt E OVR-2 GI.Y-1 Ecok. 1 EcuR. 1 CORE ± ↑ Ē↑.↓ 10A 82 85 83 84 $\overline{\mathbf{x}}$ 98

	HeLa cells		RK 13 cells		
	1 3 5 7		1 4 6 8. 2 3 5 7		
		80,0			80.0
		— 49.5			49.5
	***************************************	32.5	%! 		32.5
_	• Control of the cont	— 27.5		_	27.5
_		— 18.5			18.5
		1 2 3 5 7 -	1 2 3 4 5 6 7 - 80,0 - 49.5 - 32.5 - 27.5	1 2 4 6 7 2 3 5 7 2 3 5 7 8 80,0 - 49.5 - 32.5 - 27.5	1 2 3 4 5 6 7 2 1 3 4 5 6 7 8 80,0 - 49.5 - 32.5 - 27.5

Figure 44A

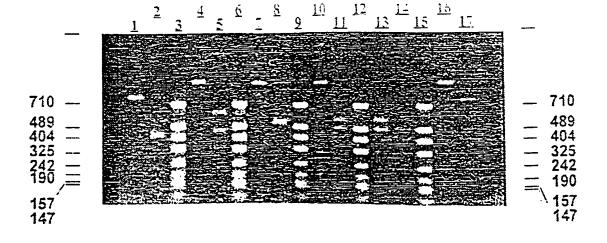






Figure 45



Figure 46